

5310
#500

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,298

DATE: 02/08/2002

TIME: 10:52:14

Input Set : A:\SO043PCTSEQ.txt

Output Set: N:\CRF3\02082002\J030298.raw

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3 <110> APPLICANT: Shionogi & Co., Ltd
5 <120> TITLE OF INVENTION: Drug for inhibiting myometrial contraction
7 <130> FILE REFERENCE: SO043PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/030,298
C--> 10 <141> CURRENT FILING DATE: 2001-12-21
11 <150> PRIOR APPLICATION NUMBER: JP P1999-177548
12 <151> PRIOR FILING DATE: 1999-06-23
13 <150> PRIOR APPLICATION NUMBER: JP P2000-79171
14 <151> PRIOR FILING DATE: 1999-03-21
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1457
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (165)..(719)
29 <220> FEATURE:
W--> 30 <221> NAME/KEY: mat peptide
31 <222> LOCATION: (447)..(602)
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36 cttggacttc ggagttttgc cattgccagt gggacgtctg agactttctc cttcaagtac 120
38 ttggcagatc actctcttag cagggctctgc gcttcgcagc cggg atg aag ctg gtt 176
39 Met Lys Leu Val
41 tcc gtc gcc ctg atg tac ctg ggt tcg ctc gcc ttc cta ggc gct gac 224
42 Ser Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp
43 -90 -85 -80 -75
45 acc gct cgg ttg gat gtc gcg tcg gag ttt cga aag aag tgg aat aag 272
46 Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys Lys Trp Asn Lys
47 -70 -65 -60
49 tgg gct ctg agt cgt ggg aag agg gaa ctg cgg atg tcc agc agc tac 320
50 Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met Ser Ser Ser Tyr
51 -55 -50 -45
53 ccc acc ggg ctc gct gac gtg aag gcc ggg cct gcc cag acc ctt att 368
54 Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala Gln Thr Leu Ile
55 -40 -35 -30
57 cgg ccc cag gac atg aag ggt gcc tct cga agc ccc gaa gac agc agt 416
58 Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro Glu Asp Ser Ser
59 -25 -20 -15
61 ccg gat gcc gcc cgc atc cga gtc aag cgc tac cgc cag agc atg aac 464
62 Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn

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63 -10          -5          -1  1          5
65 aac ttc cag ggc ctc cgg agc ttt ggc tgc cgc ttc ggg acg tgc acg 512
66 Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr
67          10          15          20
69 gtg cag aag ctg gca cac cag atc tac cag ttc aca gat aag gac aag 560
70 Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys
71          25          30          35
73 gac aac gtc gcc ccc agg agc aag atc agc ccc cag ggc tac ggc cgc 608
74 Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg
75          40          45          50
77 cgg cgc cgg cgc tcc ctg ccc gag gcc ggc ccg ggt cgg act ctg gtg 656
78 Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly Arg Thr Leu Val
79 55          60          65          70
81 tct tct aag cca caa gca cac ggg gct cca gcc ccc ccg agt gga agt 704
82 Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro Pro Ser Gly Ser
83          75          80          85
85 gct ccc cac ttt ctt taggatttag gcgcccattg tacaaggaat agtcgcgcaa 759
86 Ala Pro His Phe Leu
87          90
89 gcatcccgct ggtgacctccc gggacgaagg acttcccag cgggtgtgggg accgggctct 819
91 gacagccctg cggagacctt gagtccggga ggcaccgtcc ggcggcgagc tctggctttg 879
93 caagggcccc tccttctggg ggcttcgctt ccttagcctt gctcaggtgc aagtgcacca 939
95 gggggcgggg tgcagaagaa tccgagtgtt tgccaggctt aaggagagga gaaactgaga 999
97 aatgaatgct gagacccccg gagcaggggt ctgagccaca gccgtgctcg'cccacaaact 1059
99 gattttctcac ggcggtgtcac cccaccaggg cgcaagcctc actattactt gaactttcca 1119
101 aaacctaag aggaaaagtg caatgcgtgt tgtacataca gaggtaacta tcaatattta 1179
103 agtttgttgc tgtcaagatt tttttgttaa cttcaaatat agagatattt ttgtacgtta 1239
105 tatattgtat taagggcatt ttaaaagcaa ttatattgtc ctccccattt ttaagacgtg 1299
107 aatgtctcag cgaggtgtaa agttgttcgc cgcgtggaat gtgagtgtgt ttgtgtgcat 1359
109 gaaagagaaa gactgattac ctctgtgtg gaagaaggaa acaccgagtc tctgtataat 1419
111 ctatttacat aaaatgggtg atatgcgaac agcaaacc 1457
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115 <211> LENGTH: 185
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
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123 Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys
124          -75          -70          -65
126 Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met
127          -60          -55          -50
129 Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala
130          -45          -40          -35
132 Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro
133 -30          -25          -20          -15
135 Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
136          -10          -5          -1  1
138 Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe

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139          5          10          15
141 Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
142      20          25          30
144 Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
145 35          40          45          50
147 Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly
148          55          60          65
150 Arg Thr Leu Val Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro
151          70          75          80
153 Pro Ser Gly Ser Ala Pro His Phe Leu
154      85          90
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158 <211> LENGTH: 1493
159 <212> TYPE: DNA
160 <213> ORGANISM: Sus scrofa
162 <220> FEATURE:
163 <221> NAME/KEY: CDS
164 <222> LOCATION: (148)..(711)
166 <220> FEATURE:
W--> 167 <221> NAME/KEY: mat peptide
168 <222> LOCATION: (430)..(585)
170 <400> SEQUENCE: 3
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173 tgccactgcc agagggaagt ctcagacttc atcttcccaa atcttggcag atcaccctt 120
175 tagcagggtc tgcacatctc agccggg atg aag ctg gtt ccc gta gcc ctc atg 174
176          Met Lys Leu Val Pro Val Ala Leu Met
177          -90
179 tac ctg ggc tcg ctc gcc ttc ctg ggc gct gac aca gct cgg ctc gac 222
180 Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp Thr Ala Arg Leu Asp
181 -85          -80          -75          -70
183 gtg gcg gca gag ttc cga aag aaa tgg aat aag tgg gct cta agt cgt 270
184 Val Ala Ala Glu Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu Ser Arg
185          -65          -60          -55
187 gga aaa aga gaa ctt cgg ctg tcc agc agc tac ccc acc ggg atc gcc 318
188 Gly Lys Arg Glu Leu Arg Leu Ser Ser Ser Tyr Pro Thr Gly Ile Ala
189          -50          -45          -40
191 gac ttg aag gcc ggg cct gcc cag act gtc att cgg ccc cag gat gtg 366
192 Asp Leu Lys Ala Gly Pro Ala Gln Thr Val Ile Arg Pro Gln Asp Val
193          -35          -30          -25
195 aag ggc tcc tct cgc agc ccc cag gcc agc att ccg gat gca gcc cgc 414
196 Lys Gly Ser Ser Arg Ser Pro Gln Ala Ser Ile Pro Asp Ala Ala Arg
197          -20          -15          -10
199 atc cga gtc aag cgc tac cgc cag agt atg aac aac ttc cag ggc ctg 462
200 Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Asn Phe Gln Gly Leu
201 -5          -1 1          5          10
203 cgg agc ttc ggc tgt cgc ttt ggg acg tgc acc gtg cag aag ctg gcg 510
204 Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala
205          15          20          25
207 cac cag atc tac cag ttc acg gac aaa gac aag gac ggc gtc gcc ccc 558

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208 His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Val Ala Pro
209          30          35          40
211 cgg agc aag atc agc ccc cag ggc tac ggc cgc cgg cgc cga cgc tct 606
212 Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Arg Ser
213          45          50          55
215 ctg ccc gaa gcc agc ctg ggc cgg act ctg agg tcc cag gag cca cag 654
216 Leu Pro Glu Ala Ser Leu Gly Arg Thr Leu Arg Ser Gln Glu Pro Gln
217 60          65          70          75
219 gcg cac ggg gcc ccg gcc tcc ccg gcg cat caa gtg ctc gcc act ctc 702
220 Ala His Gly Ala Pro Ala Ser Pro Ala His Gln Val Leu Ala Thr Leu
221          80          85          90
223 ttt agg att taggcgccta ctgtggcagc agcgaacagt cgcgcacatgca 751
224 Phe Arg Ile
226 tcatgccggc gcttcctggg gcggggggct tcccggagcc gagccccctca gcggctgggg 811
228 cccgggcaga gacagcattg agagaccgag agtccgggag gcacagacca gcggcgagcc 871
230 ctgcattttc aggaaccgt cctgcttgga ggcagtgttc tcttcggctt aatccagccc 931
232 ggggtccccg gtgggggtgg aggggtgcaga ggaatccaaa ggagtgtcat ctgccaggct 991
234 cacggagagg agaaactgcg aagtaaattgc ttagaccccc aggggcaagg gtctgagcca 1051
236 ctgcctgtgc gccacaaaac tgatttctga aggggaataa cccaacagg gcgcaagcct 1111
238 cactattact tgaactttcc aaaacctaga gaggaaggat gcaatgtatg ttgtatataa 1171
240 agaggtaact atcaatattt aagtttgttg ctgtcaagat ttttttttgt aacttcaaat 1231
242 atagagatat ttttgtacgt tatatattgt attaagggca ttttaaaaca attgtattgt 1291
244 tccccctccc totattttta tatgtgaatg tctcagcgag gtgtaacatt gtttgctgcg 1351
246 cgaaatgtga gagtgtgtgt gtgtgtgtgc gtgaaagaga gtctggatgc ctcttgggga 1411
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254 <211> LENGTH: 188
255 <212> TYPE: PRT
256 <213> ORGANISM: Sus scrofa
258 <400> SEQUENCE: 4
259 Met Lys Leu Val Pro Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe
260          -90          -85          -80
262 Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ala Glu Phe Arg Lys
263          -75          -70          -65
265 Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Leu
266          -60          -55          -50
268 Ser Ser Ser Tyr Pro Thr Gly Ile Ala Asp Leu Lys Ala Gly Pro Ala
269          -45          -40          -35
271 Gln Thr Val Ile Arg Pro Gln Asp Val Lys Gly Ser Ser Arg Ser Pro
272 -30          -25          -20          -15
274 Gln Ala Ser Ile Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
275          -10          -5          -1 1
277 Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
278          5          10          15
280 Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
281          20          25          30
283 Asp Lys Asp Lys Asp Gly Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
284 35          40          45          50

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Input Set : A:\SO043PCTSEQ.txt

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286 Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu Pro Glu Ala Ser Leu Gly
287                      55                      60                      65
289 Arg Thr Leu Arg Ser Gln Glu Pro Gln Ala His Gly Ala Pro Ala Ser
290                      70                      75                      80
292 Pro Ala His Gln Val Leu Ala Thr Leu Phe Arg Ile
293                      85                      90
296 <210> SEQ ID NO: 5
297 <211> LENGTH: 1376
298 <212> TYPE: DNA
299 <213> ORGANISM: Rattus norvegicus
301 <220> FEATURE:
302 <221> NAME/KEY: CDS
303 <222> LOCATION: (154)..(708)
305 <220> FEATURE:
W--> 306 <221> NAME/KEY: mat peptide
307 <222> LOCATION: (433)..(582)
309 <400> SEQUENCE: 5
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312 ggttttgccg ctgtcagaag gacgtctcgg actttctgct tcaagtgctt gacaactcac 120
314 cctttcagca gggatcggga gcatcgctac aga atg aag ctg gtt tcc atc gcc 174
315                      Met Lys Leu Val Ser Ile Ala
316                      -90
318 ctg atg tta ttg ggt tcg ctc gcc gtt ctc ggc gcg gac acc gca cgg 222
319 Leu Met Leu Leu Gly Ser Leu Ala Val Leu Gly Ala Asp Thr Ala Arg
320 -85                      -80                      -75
322 ctc gac act tcc tcg cag ttc cga aag aag tgg aat aag tgg gcg cta 270
323 Leu Asp Thr Ser Ser Gln Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu
324 -70                      -65                      -60                      -55
326 agt cgt ggg aag agg gaa cta caa gcg tcc agc agc tac cct acg ggg 318
327 Ser Arg Gly Lys Arg Glu Leu Gln Ala Ser Ser Ser Tyr Pro Thr Gly
328                      -50                      -45                      -40
330 ctc gtt gat gag aag aca gtc ccg acc cag act ctt ggg ctc cag gac 366
331 Leu Val Asp Glu Lys Thr Val Pro Thr Gln Thr Leu Gly Leu Gln Asp
332                      -35                      -30                      -25
334 aag cag agc acg tct agc acc cca caa gcc agc act cag agc aca gcc 414
335 Lys Gln Ser Thr Ser Ser Thr Pro Gln Ala Ser Thr Gln Ser Thr Ala
336                      -20                      -15                      -10
338 cac att cga gtc aaa cgc tac cgc cag agc atg aac cag ggg tcc cgc 462
339 His Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Gln Gly Ser Arg
340 -5                      -1 1                      5                      10
342 agc act gga tgc cgc ttt ggg acc tgc aca atg cag aaa ctg gct cac 510
343 Ser Thr Gly Cys Arg Phe Gly Thr Cys Thr Met Gln Lys Leu Ala His
344                      15                      20                      25
346 cag atc tac cag ttt aca gac aaa gac aag gac ggc atg gcc ccc aga 558
347 Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Met Ala Pro Arg
348                      30                      35                      40
350 aac aag atc agc cct caa ggc tat ggc cgc cgg cgc cgg cgt tcc ctg 606
351 Asn Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu
352                      45                      50                      55

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/030,298

DATE: 02/08/2002

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Input Set : A:\S0043PCTSEQ.txt

Output Set: N:\CRF3\02082002\J030298.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:306 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5